

110> APPLICANT: KUWABARA, Yoko  
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MORI, Yukiko  
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#4

120> TITLE OF INVENTION: CARBAMOYL-PHOSPHATE SYNTHETASE GENE OF CORYNEFORM  
BACTERIA AND METHOD FOR PRODUCING L-ARGININE  
130> FILE REFERENCE: OP945CIP  
140> CURRENT APPLICATION NUMBER: US/09/629,616  
141> CURRENT FILING DATE: 2000-07-31  
160> NUMBER OF SEQ ID NOS: 7  
170> SOFTWARE: PatentIn Ver. 2.0

210> SEQ ID NO 1  
211> LENGTH: 4837  
212> TYPE: DNA  
213> ORGANISM: Brevibacterium lactofermentum  
220> FEATURE:  
221> NAME/KEY: CDS  
222> LOCATION: (283)..(1461)  
221> NAME/KEY: CDS  
222> LOCATION: (1470)..(4808)  
400> SEQUENCE: 1

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gcattgcata taatgcaatg aattgaataa actacattca ggttatcaa ccagccaatt 240
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Tyr Gln Glu Thr Met Thr Asp Pro Ser Tyr His Arg Gln Ile Val Val
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Leu Ala Tyr Asn Thr Glu Asp Leu Glu Arg Ile Ala Gly Gly Gly Leu			
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Ala Ala Ser Pro Glu Ala Asn Val Leu Ile Glu Glu Ser Ile Leu Gly			
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Trp Lys Glu Phe Glu Leu Glu Leu Met Arg Asp Thr Ala Asp Asn Val			
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gtg gtt atc tgc tcc att gaa aac gtc gac gca ctg ggc gtg cac acc			2216
Val Val Ile Cys Ser Ile Glu Asn Val Asp Ala Leu Gly Val His Thr			
235	240	245	
ggc gac tct gtc acc gtg gca cct gcc ctg acc ctg act gac cgt gaa			2264
Gly Asp Ser Val Thr Val Ala Pro Ala Leu Thr Leu Thr Asp Arg Glu			
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ttc cag aag atg cgc gat cag ggt atc gcc atc atc cgc gag gtc ggc			2312
Phe Gln Lys Met Arg Asp Gln Gly Ile Ala Ile Ile Arg Glu Val Gly			
270	275	280	
gtg gac acc ggt gga tgt aac atc cag ttc gct atc aac cca gtt gat			2360
Val Asp Thr Gly Cys Asn Ile Gln Phe Ala Ile Asn Pro Val Asp			
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Gly Arg Ile Ile Thr Ile Glu Met Asn Pro Arg Val Ser Arg Ser Ser			
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Ala Leu Ala Ser Lys Ala Thr Gly Phe Pro Ile Ala Lys Met Ala Ala			
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Lys Leu Ala Ile Gly Tyr Thr Leu Asp Glu Ile Thr Asn Asp Ile Thr			
330	335	340	345
ggt gaa acc cca gct gcg ttt gag ccc acc atc gac tac gtc gtg gtc			2552
Gly Glu Thr Pro Ala Ala Phe Glu Pro Thr Ile Asp Tyr Val Val Val			
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Lys Ala Pro Arg Phe Ala Phe Glu Lys Phe Val Gly Ala Asp Asp Thr			
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ttg acc acc acc atg aag tcc gtc ggt gag gtc atg tcc ctg ggc cgt			2648
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Asn Tyr Ile Ala Ala Leu Asn Lys Ala Leu Arg Ser Leu Glu Thr Lys			
395	400	405	
cag cag ggt ttc tgg acc aag cct gat gag ttc ttc gca ggg gag cgc			2744
Gln Gln Gly Phe Trp Thr Lys Pro Asp Glu Phe Phe Ala Gly Glu Arg			
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gct acc gat aag gca gct gtt ctg gaa gat ctc aag cgc cca acc gaa			2792
Ala Thr Asp Lys Ala Ala Val Leu Glu Asp Leu Lys Arg Pro Thr Glu			
430	435	440	
ggc cgc ctc tac gac gtt gag ctg gca atg cgc ctt ggc gca agc gtg			2840
Gly Arg Leu Tyr Asp Val Glu Leu Ala Met Arg Leu Gly Ala Ser Val			
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Glu Glu Leu Tyr Glu Ala Ser Ser Ile Asp Pro Trp Phe Leu Ala Glu			
460	465	470	
ctt gaa gct ctc gtg cag ttc cgc cag aag ctc gtt gac gca cca ttc			2936
Leu Glu Ala Leu Val Gln Phe Arg Gln Lys Leu Val Asp Ala Pro Phe			
475	480	485	
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Leu Asn Glu Asp Leu Leu Arg Glu Ala Lys Phe Met Gly Leu Ser Asp			

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Leu Gln Ile Ala Ala Leu Arg Pro Glu Phe Ala Gly Glu Asp Gly Val		
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cgc acc ttg cgt ctg tcc cta ggc atc cgc cca gta ttc aag act gtc	3080	
Arg Thr Leu Arg Leu Ser Leu Gly Ile Arg Pro Val Phe Lys Thr Val		
525	530	535
gat acc tgt gca gca gag ttt gaa gct aag act ccg tac cac tac tcc	3128	
Asp Thr Cys Ala Ala Glu Phe Glu Ala Lys Thr Pro Tyr His Tyr Ser		
540	545	550
gca tac gag ctg gat cca gca gct gag tct gag gtc gca cca cag act	3176	
Ala Tyr Glu Leu Asp Pro Ala Ala Glu Ser Glu Val Ala Pro Gln Thr		
555	560	565
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Glu Arg Glu Lys Val Leu Ile Leu Gly Ser Gly Pro Asn Arg Ile Gly		
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Gln Gly Ile Glu Phe Asp Tyr Ser Cys Val His Ala Ala Leu Glu Leu		
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Ser Arg Val Gly Tyr Glu Thr Val Met Val Asn Cys Asn Pro Glu Thr		
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gtg tcc acc gac tac gac acc gct gac cgc ctg tac ttc gag cca ctg	3368	
Val Ser Thr Asp Tyr Asp Thr Ala Asp Arg Leu Tyr Phe Glu Pro Leu		
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Thr Phe Glu Asp Val Met Glu Val Tyr His Ala Glu Ala Gln Ser Gly		
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cca gag gca atc gac atg gct gag gac cgt ggc gag ttc ggt gca ctg	3560	
Pro Glu Ala Ile Asp Met Ala Glu Asp Arg Gly Glu Phe Gly Ala Leu		
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ctg aac cgc gag cag ctt cct gct cca gca ttc ggc acc gca acc tct	3608	
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Phe Glu Glu Ala Arg Thr Val Ala Asp Glu Ile Ser Tyr Pro Val Leu		
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gtt cgc cct tcc tac gtc ttg ggt ggc cgt ggc atg gag att gtc tac	3704	
Val Arg Pro Ser Tyr Val Leu Gly Gly Arg Gly Met Glu Ile Val Tyr		
730	735	740
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Asp Glu Ala Ser Leu Glu Asp Tyr Ile Asn Arg Ala Thr Glu Leu Ser		
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Ser Asp His Pro Val Leu Val Asp Arg Phe Leu Asp Asn Ala Ile Glu		
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Ile Asp Val Asp Ala Leu Cys Asp Gly Asp Glu Val Tyr Leu Ala Gly		
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Val Met Glu His Ile Glu Glu Ala Gly Ile His Ser Gly Asp Ser Ala		
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tgt gca ctt cct cca atg act ttg ggc gca cag gac atc gag aag gtc	3944	
Cys Ala Leu Pro Pro Met Thr Leu Gly Ala Gln Asp Ile Glu Lys Val		
810	815	820
cgc gaa gca acc aag ctg gct ctg ggc atc ggc gta cag ggc ctg	3992	
Arg Glu Ala Thr Lys Lys Leu Ala Leu Gly Ile Gly Val Gln Gly Leu		
830	835	840
atg aac gtc cag tac gca ctc aag gac gac atc ctc tac gtc atc gag	4040	
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gat	tgt	gaa	ggt	gtg	ctc	aag	gct	tcc	gac	atc	cgc	gaa	ggt	gta	gag	4568														
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<210> SEQ ID NO 2  
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 <212> TYPE: PRT  
 <213> ORGANISM: Brevibacterium lactofermentum  
 <400> SEQUENCE: 2

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Gly	Phe	Gly	Ala	Ile	Gly	Thr	Thr	Leu	Gly	Glu	Ala	Val	Phe	Thr	Thr
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Ala	Met	Thr	Gly	Tyr	Gln	Glu	Thr	Met	Thr	Asp	Pro	Ser	Tyr	His	Arg
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Gln	Ile	Val	Val	Ala	Thr	Ala	Pro	Gln	Ile	Gly	Asn	Thr	Gly	Trp	Asn
65					70				75						80

Asp	Glu	Asp	Asn	Glu	Ser	Arg	Asp	Gly	Lys	Ile	Trp	Val	Ala	Gly	Leu
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Val	Ile	Arg	Asp	Leu	Ala	Ala	Arg	Val	Ser	Asn	Trp	Arg	Ala	Thr	Thr
			100					105					110		
Ser	Leu	Gln	Gln	Glu	Met	Ala	Asp	Gln	Gly	Ile	Val	Gly	Ile	Gly	Gly
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Ile	Asp	Thr	Arg	Ala	Leu	Val	Arg	His	Leu	Arg	Asn	Glu	Gly	Ser	Ile
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Ala	Ala	Gly	Ile	Phe	Ser	Gly	Ala	Asp	Ala	Gln	Arg	Pro	Val	Glu	Glu
145				150						155				160	
Leu	Val	Glu	Ile	Val	Lys	Asn	Gln	Pro	Ala	Met	Thr	Gly	Ala	Asn	Leu
			165						170					175	
Ser	Val	Glu	Val	Ser	Ala	Asp	Glu	Thr	Tyr	Val	Ile	Glu	Ala	Glu	Gly
			180					185					190		
Glu	Glu	Arg	His	Thr	Val	Val	Ala	Tyr	Asp	Leu	Gly	Ile	Lys	Gln	Asn
	195						200					205			
Thr	Pro	Arg	Arg	Phe	Ser	Ala	Arg	Gly	Val	Arg	Thr	Val	Ile	Val	Pro
	210					215					220				
Ala	Glu	Thr	Pro	Leu	Glu	Asp	Ile	Lys	Gln	Tyr	Asn	Pro	Ser	Gly	Val
225					230					235					240
Phe	Ile	Ser	Asn	Gly	Pro	Gly	Asp	Pro	Ala	Ala	Ala	Asp	Val	Met	Val
			245						250					255	
Asp	Ile	Val	Arg	Glu	Val	Leu	Glu	Ala	Asp	Ile	Pro	Phe	Phe	Gly	Ile
		260						265				270			
Cys	Phe	Gly	Asn	Gln	Ile	Leu	Gly	Arg	Ala	Phe	Gly	Met	Glu	Thr	Tyr
	275						280					285			
Lys	Leu	Lys	Phe	Gly	His	Arg	Gly	Ile	Asn	Val	Pro	Val	Lys	Asn	His
	290					295				300					
Ile	Thr	Gly	Lys	Ile	Asp	Ile	Thr	Ala	Gln	Asn	His	Gly	Phe	Ala	Leu
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Lys	Gly	Glu	Ala	Gly	Gln	Glu	Phe	Glu	Thr	Asp	Phe	Gly	Thr	Ala	Ile
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Val	Thr	His	Thr	Cys	Leu	Asn	Asp	Gly	Val	Val	Glu	Gly	Val	Ala	Leu
			340					345					350		
Lys	Ser	Gly	Arg	Ala	Tyr	Ser	Val	Gln	Tyr	His	Pro	Glu	Ala	Ala	Ala
		355					360					365			
Gly	Pro	Asn	Asp	Ala	Ser	Pro	Leu	Phe	Asp	Gln	Phe	Val	Glu	Leu	Met
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<210> SEQ ID NO 3  
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 <212> TYPE: PRT  
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		20						25					30		
Ala	Cys	Arg	Val	Leu	Lys	Glu	Glu	Gly	Leu	Arg	Val	Thr	Leu	Ile	Asn
		35				40						45			
Ser	Asn	Pro	Ala	Thr	Ile	Met	Thr	Asp	Pro	Glu	Met	Ala	Asp	His	Thr
	50					55				60					
Tyr	Val	Glu	Pro	Ile	Glu	Pro	Glu	Tyr	Ile	Asp	Lys	Ile	Phe	Ala	Lys
	65				70				75					80	
Glu	Ile	Glu	Gln	Gly	His	Pro	Ile	Asp	Ala	Val	Leu	Ala	Thr	Leu	Gly
			85						90					95	
Gly	Gln	Thr	Ala	Leu	Asn	Ala	Ala	Ile	Gln	Leu	Asp	Arg	Leu	Gly	Ile
		100						105					110		
Leu	Glu	Lys	Tyr	Gly	Val	Glu	Leu	Ile	Gly	Ala	Asp	Ile	Asp	Ala	Ile
		115				120					125				
Glu	Arg	Gly	Glu	Asp	Arg	Gln	Lys	Phe	Lys	Asp	Ile	Val	Thr	Thr	Ile
	130					135					140				
Gly	Gly	Glu	Ser	Ala	Arg	Ser	Arg	Val	Cys	His	Asn	Met	Asp	Glu	Val
145					150					155					160

His Glu Thr Val Ala Glu Leu Gly Leu Pro Val Val Val Arg Pro Ser  
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 Phe Thr Met Gly Gly Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu Asp  
 180 185 190  
 Leu Glu Arg Ile Ala Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala Asn  
 195 200 205  
 Val Leu Ile Glu Glu Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu Glu  
 210 215 220  
 Leu Met Arg Asp Thr Ala Asp Asn Val Val Val Ile Cys Ser Ile Glu  
 225 230 235 240  
 Asn Val Asp Ala Leu Gly Val His Thr Gly Asp Ser Val Thr Val Ala  
 245 250 255  
 Pro Ala Leu Thr Leu Thr Asp Arg Glu Phe Gln Lys Met Arg Asp Gln  
 260 265 270  
 Gly Ile Ala Ile Ile Arg Glu Val Gly Val Asp Thr Gly Gly Cys Asn  
 275 280 285  
 Ile Gln Phe Ala Ile Asn Pro Val Asp Gly Arg Ile Ile Thr Ile Glu  
 290 295 300  
 Met Asn Pro Arg Val Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala Thr  
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 Gly Phe Pro Ile Ala Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr Thr  
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 Leu Asp Glu Ile Thr Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala Phe  
 340 345 350  
 Glu Pro Thr Ile Asp Tyr Val Val Val Lys Ala Pro Arg Phe Ala Phe  
 355 360 365  
 Glu Lys Phe Val Gly Ala Asp Asp Thr Leu Thr Thr Thr Met Lys Ser  
 370 375 380  
 Val Gly Glu Val Met Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu Asn  
 385 390 395 400  
 Lys Ala Leu Arg Ser Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr Lys  
 405 410 415  
 Pro Asp Glu Phe Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala Val  
 420 425 430  
 Leu Glu Asp Leu Lys Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val Glu  
 435 440 445  
 Leu Ala Met Arg Leu Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala Ser  
 450 455 460  
 Ser Ile Asp Pro Trp Phe Leu Ala Glu Leu Glu Ala Leu Val Gln Phe  
 465 470 475 480  
 Arg Gln Lys Leu Val Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu Arg  
 485 490 495  
 Glu Ala Lys Phe Met Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu Arg  
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 Pro Glu Phe Ala Gly Glu Asp Gly Val Arg Thr Leu Arg Leu Ser Leu  
 515 520 525  
 Gly Ile Arg Pro Val Phe Lys Thr Val Asp Thr Cys Ala Ala Glu Phe  
 530 535 540  
 Glu Ala Lys Thr Pro Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro Ala  
 545 550 555 560  
 Ala Glu Ser Glu Val Ala Pro Gln Thr Glu Arg Glu Lys Val Leu Ile  
 565 570 575  
 Leu Gly Ser Gly Pro Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp Tyr  
 580 585 590  
 Ser Cys Val His Ala Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu Thr  
 595 600 605  
 Val Met Val Asn Cys Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp Thr  
 610 615 620  
 Ala Asp Arg Leu Tyr Phe Glu Pro Leu Thr Phe Glu Asp Val Met Glu  
 625 630 635 640  
 Val Tyr His Ala Glu Ala Gln Ser Gly Thr Val Ala Gly Val Ile Val  
 645 650 655  
 Gln Leu Gly Gly Gln Thr Pro Leu Gly Leu Ala Asp Arg Leu Lys Lys  
 660 665 670  
 Ala Gly Val Pro Val Ile Gly Thr Ser Pro Glu Ala Ile Asp Met Ala  
 675 680 685

Glu Asp Arg Gly Glu Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu Pro  
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 Ala Pro Ala Phe Gly Thr Ala Thr Ser Phe Glu Ala Arg Thr Val  
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 Ala Asp Glu Ile Ser Tyr Pro Val Leu Val Arg Pro Ser Tyr Val Leu  
 725 730 735  
 Gly Gly Arg Gly Met Glu Ile Val Tyr Asp Glu Ala Ser Leu Glu Asp  
 740 745 750  
 Tyr Ile Asn Arg Ala Thr Glu Leu Ser Ser Asp His Pro Val Leu Val  
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 Asp Arg Phe Leu Asp Asn Ala Ile Glu Ile Asp Val Asp Ala Leu Cys  
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 Asp Gly Asp Glu Val Tyr Leu Ala Gly Val Met Glu His Ile Glu Glu  
 785 790 795 800  
 Ala Gly Ile His Ser Gly Asp Ser Ala Cys Ala Leu Pro Pro Met Thr  
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 Leu Gly Ala Gln Asp Ile Glu Lys Val Arg Glu Ala Thr Lys Lys Leu  
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 Ala Leu Gly Ile Gly Val Gln Gly Leu Met Asn Val Gln Tyr Ala Leu  
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 Lys Asp Asp Ile Leu Tyr Val Ile Glu Ala Asn Pro Arg Ala Ser Arg  
 850 855 860  
 Thr Val Pro Phe Val Ser Lys Ala Thr Gly Val Asn Leu Ala Lys Ala  
 865 870 875 880  
 Ala Ser Arg Ile Ala Val Gly Ala Thr Ile Lys Asp Leu Gln Asp Glu  
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 Gly Met Ile Pro Thr Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp Ala  
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 Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Asn Arg Phe Arg Arg  
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 Pro Asp Gly Lys Thr Leu Asp Thr Leu Leu Ser Pro Glu Met Lys Ser  
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 Thr Gly Glu Val Met Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr Ala  
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 Phe Val Thr Val Ala Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro Ile  
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 Gln Arg Leu Ala Ser Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly Thr  
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 Ala Ser Asp Ile Arg Glu Gly Val Glu Gly Lys Ser Ile Val Asp Arg  
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